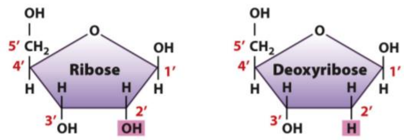
Chromosomal structure:

| Bacteria | Eukaryote |
|---|---|
| Circular | Linear |
| Haploid | Diploid |
| Double-stranded | Double-stranded |

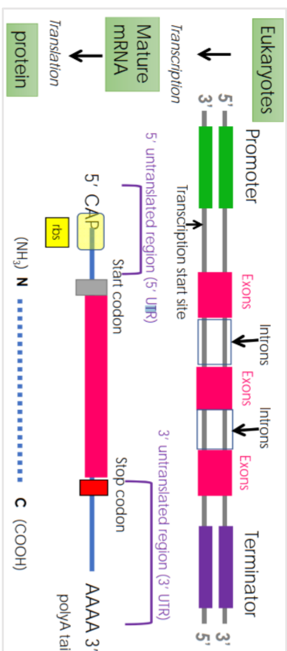
**Nucleic acids**

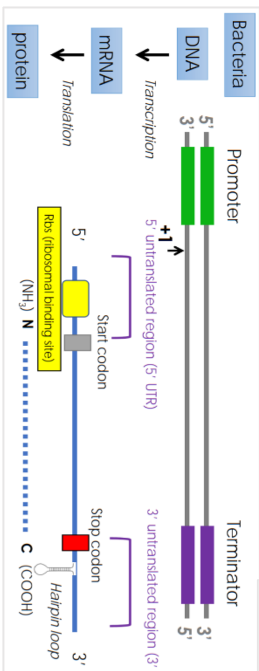
- Purines (A,G) pair with pyrimidines (T,C)
- A-T and G-C allow same geometry
- A and T are held together by **2** H-bonds, while G and C are held by **3**




**Transcription**

- start at +1 site nucleotide
- template read 3'→5'
- mRNA made goes from 5'→3'
- writing mRNA convention: **N**-meth…-**C**
- mRNA identical to coding strand, **T** replaced by **U**




**RNA Pol and Promoter in Bac and Euk**

1) In Bac:

- **Sigma protein** binds to -10 and -35 box to help recruit RNA Pol. "HOLOENZYME"
- terminated by **hairpin loop** on mRNA, causing RNA Pol to dissociate.

2) In Euk:

- **TBP** (TATA binding protein) & General Transcription Factors bind to promoter to recruit binding of RNA Pol

**DNA binding proteins:**

- bind in major & minor grooves
- bind by H-bonds and non-covalent bond
- promoters closer to consensus sequence (**strong promoters)** bind RNA Pol more often and more tightly
- **Strong promoters -** closer to consensus

**RNA processing:**

1) Addition of 5' CAP; 2) Polyadenylation (forming Poly A tail); 3) splicing introns and exons

- CAP and tail aid in transport across nuclear membrane, increases stability, protects from degradation, help promote translation – recognized by ribosome for binding.
- splicing (in nucleus) by **spliceosomes**. Cut at splice junctions and link exons tgt.
- **Alternative Splicing** creates **splice variants** – more than 1 type of protein can be made


- **Open reading frame** – part of the gene being translated. Starts with start codon

**Translation**

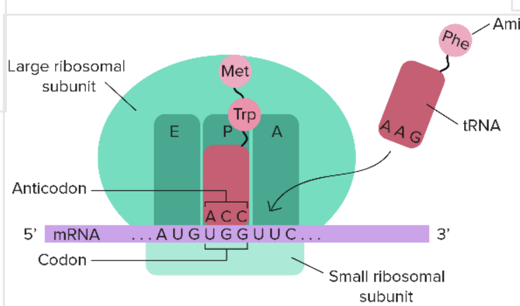
- anti-codon on tRNA are anti-parallel and complementary to codon on mRNA
- redundancy – more than 1 codon codes for an amino acid.
- "Wobble effect" – multiple codons can bind to a single tRNA. tRNA can bind if the first 2 bases match.
- ribosomes move from 5'→3' of mRNA

Steps: 1) small ribosomal subunit (80S in Euk, 70S in Bac) binds to rbs site (in Euk is 5' CAP, in Bac by complementary base pair). $tRNA^{meth}$ binds to start codon.

2) large subunit assembles ($tRNA^{meth}$ in P site first)

3) New charged tRNA comes in A site. Peptide bond between 2 amino acids. Bond between old tRNA and AA is cleaved & ribosomes move along mRNA by 1 codon

4) Old tRNA is released in E site.




- **Aminoacyl tRNA synthetase** is an enzyme that attaches a tRNA with a specific AA. Each AA has one enzyme.

+ Remember when analysing micrographs, Euk shows translation only (mRNA only) while Bac shows both translation and transcription at the same time (both DNA and mRNA)

**Operons, operators, promoters…**

- strong promoters are closer to consensus
- Operon includes a promoter, terminator, and coding sequences

| Positive regulation | Negative regulation |
|---|---|
| Regulatory protein – activator protein – binds to a region close to promoter (operator) and increase transcription | Regulatory protein – repressor protein – binds to region close to promoter and decrease transcription |
| Eg: MalT | Eg: LacI |

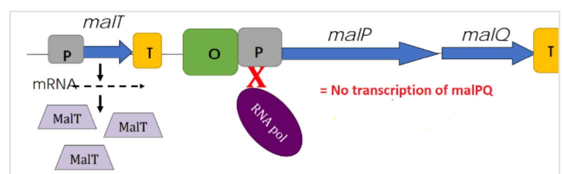
Gene and protein writing convention:

- Genes: no caps, underlined. Eg: malP, malQ, malT
- Proteins: caps. Eg: MalP, MalQ

**Maltose operon regulation:**

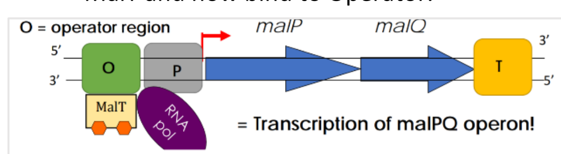
- MalT is **positive** regulator of malPQ operon. Promoter of malPQ is weak and further from consensus. Signal molecule is maltose.
- MalP and MalQ are enzymes used to break down maltose → glucose
- MalT **always** available in small amounts in cytoplasm but can't bind to operator alone.

1) No maltose scenario:



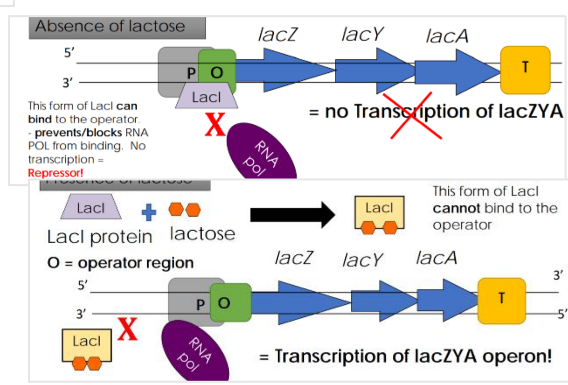

2) Maltose present scenario:

- Maltose bind to MalT → changes shape MalT and now bind to Operator.

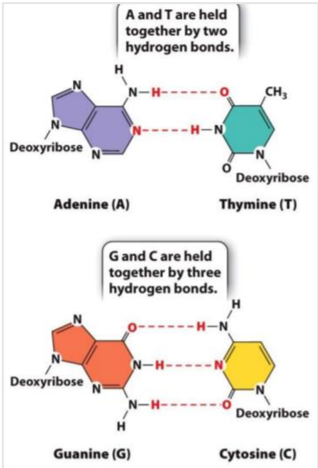



**Lactose operon regulation:**

- LacI is **negative** regulator of lacZYA operon. Promoter of lacZYA is **strong** and closer to consensus. Like MalT, LacI also has own promoter, terminator and coding region.
- Operator is found downstream but overlapping promoter.



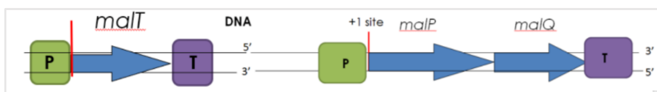
**Other info:**




| Gene structure | Bacterial Gene? √ | Eukaryotic gene? √ | Function |
|---|---|---|---|
| Promoter | √ | √ | Binds the RNA Polymerase |
| Introns | | √ | Sequence that are cut out in RNA processing/splicing |
| Stop codon | | | TRANSLATION! |
| 5' CAP | | √ | Added to mRNA AFTER synthesized |
| TATA box | | √ | sequence on Euk promoter |
| -10 and -35 box | √ | | sequence on Bac promoter |
| Template strand | √ | √ | Codes for the mRNA |
| Transcription start site | √ (+1 site) | √ | First base that is transcribed into mRNA<br>Bac = ~10 bases from -10 box<br>Euk = ~25 bases from TATA box |
| Terminator | √ (hairpin) | √ | Terminates transcription –<br>Bac = hairpin loop, Euk – multiple repeat sequences |
| +1 site | √ | | First base that is transcribed into mRNA |
| Start codon | | | TRANSLATION! |
| Exons | | √ | Coding regions that may be spliced out or kept in a mRNA transcript. |
| Ribosomal binding site | | | TRANSLATION! |
| Non-template /coding | √ | √ | Opposite strand of the template but often used to read the code! |
| Poly A tail | | √ | Added after mRNA made in Euk. |

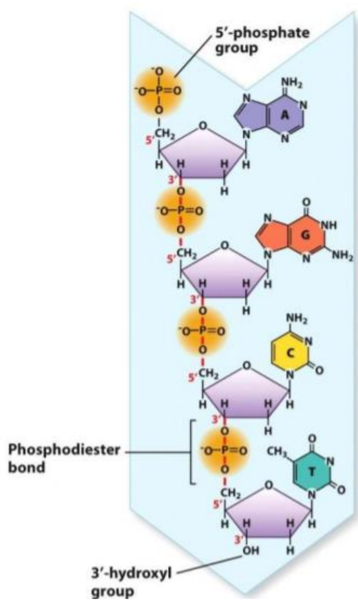
- Genome is all genetic material of organism
- Genotype is genetic make-up of organism
- Phenotype is characteristics
- There's little correlation between genome size, the number of genes and the complexity of an organism.

**For something like this:**




- Each gene requires its own **start codon and ribosome binding sites**.
- Only need 1 RNA Pol for each promoter
- Terminator sequence doesn't stop translation for all proteins.

**DNA Strand:**




- New nucleotide added to 3' end.

- Genetic code is redundant→many codons code for one amino acid

**Bonding:**

| | Bond type | Example? |
|---|---|---|
| | Covalent | Strongest |
| | Ionic | |
| Non-covalent | Ion – Permanent Dipole (IPD) | |
| Non-covalent | Permanent Dipole – Permanent Dipole (PDPD) | |
| Non-covalent | Permanent Dipole – Induced Dipole (PDID) | |
| Non-covalent | Induced Dipole – Induced Dipole (IDID) | weakest |